

1 GCACGAGGAACAGAACACTTTCTCATGTCCAGGGTCAGATTACAAGAGCACTCAAGACTT 60
 61 TACTGACGAAAACCTCAGGAAATCCTCTATCACAAAGAGGTTTGGCAACTAACTAAGACA 120
 121 TTAAAAGGAAAATACCAGATGCCACTCTGCAGGCTGCAATAACTACTACTTACTGGATAC 180
 181 ATTCAAACCCTCCAGAATCAACAGTTATCAGGTAACCAACAAGAAATGCAAGCCGTCGAC 240
 1 M Q A V D 5
 241 AATCTCACCTCTGCGCCTGGGAACACCAGTCTGTGCACCAGAGACTACAAAATCACCCAG 300
 6 N L T S A P G N T S L C T R D Y K I T Q 25
 301 GTCCTCTTCCCACTGCTCTACACTGTCCTGTTTTTGTGGACTTATCACAAATGGCCTG 360
 26 V L F P L L Y T V L F F V G L I T N G L 45
 361 GCGATGAGGATTTTCTTTCAAATCCGGAGTAAATCAAACCTTTATTATTTTCTTAAGAAC 420
 46 A M R I F F Q I R S K S N F I I F L K N 65
 421 ACAGTCATTTCTGATCTTCTCATGATTCTGACTTTTCCATTCAAATCTTAGTGATGCC 480
 66 T V I S D L L M I L T F P F K I L S D A 85
 481 AAACGGGAACAGGACCACTGAGAACTTTTGTGTGTCAAGTTACCTCCGTCATATTTTAT 540
 86 K L G T G P L R T F V C Q V T S V I F Y 105
 541 TTCACAATGTATATCAGTATTTTCTTCTGGGACTGATAACTATCGATCGCTACCAGAAG 600
 106 F T M Y I S I S F L G L I T I D R Y Q K 125
 601 AcCACCAGGCCATTTAAAACATCCAACCCCAAAAATCTCTTGGGGGCTAAGATTCTCTCT 660
 126 T T R P F K T S N P K N L L G A K I L S 145
 661 GTTGTCTCTGGGCATTCATGTTCTTACTCTCTTtGCCTAACATGATTCTGACCAACAGg 720
 146 V V I W A F M F L L S L P N M I L T N R 165
 721 CAGCCGAGAGACAAGAATGTGaAGAAaTGCTCTTTCCTTAAATCAGAGTTCGGTCTAGTC 780
 166 Q P R D K N V K K C S F L K S E F G L V 185
 781 TGGCATGAAATAGTAAATTACATCTGTCAAGTCATTTTCTGGATTAATTTCTTAATTGTT 840
 186 W H E I V N Y I C Q V I F W I N F L I V 205

FIG.1A

841 ATTGTATGTTATACACTCATTACAAAAGAACTGTACCGGTCATACGTAAGAACGAGGGGT 900
206 I V C Y T L I T K E L Y R S Y V R T R G 225

901 GTAGGTAAAGTCCCCAGGAAAAAGGTGAACGTCAAAGTTTTTCATTATCATTGCTGTATTC 960
226 V G K V P R K K V N V K V F I I I A V F 245

961 TTTATTTGTTTTGTTCTTTCCATTTTGCCCGAATTCCTTACACCCTGAGCCAAACCCGG 1020
246 F I C F V P F H F A R I P Y T L S Q T R 265

1021 GATGTCTTTGACTGCACtGcTGAAAATACTCTGTTCTATGTGAAAGAGAGCACTCTGTGG 1080
266 D V F D C T A E N T L F Y V K E S T L W 285

1081 TTAAGTTCCTTAAATGCATGCCTGGATCCGTTTCATCTATTTTTTCTTTGCAAGTCCTTC 1140
286 L T S L N A C L D P F I Y F F L C K S F 305

1141 AGAAATTCCTTGATAAGTATGCTGAAGTGCCCAATTCTGCAACATCTCTGTCCCAGGAC 1200
306 R N S L I S M L K C P N S A T S L S Q D 325

1201 AATAGGAAAAAAGAACAGGATGGTGGTGAcCCAAATGAAGAGACTCCAATGTAAACAAAT 1260
326 N R K K E Q D G G D P N E E T P M * 343

1261 TAACTAAGGAAATATTTCAATCTCTTTGTGTTCAGAACTCGTTAAAGCAAAGCGCTAAGT 1320

1321 AAAAAATTAAGTACGAGGAAGCAACTAAGTTAATAATAATGACTCTAAAGAAACAGAA 1380

1381 GATTACAAAAGCAATTTTCATTTACCTTTCCAGTATGAAAAGCTATCTTAAATATAGAA 1440

1441 AACTAATCTAACTGTAGCTGTATTAGCAGCAAAACAAACGACATCCAATTGTCATGCTG 1500

1501 CATGCAAACTACACAGAATTCATGTTTTGgCAGAGTTTTGGCAAAATGAGTAATCATAT 1560

1561 AATATTTACTGTAATTTTTTAAAATACATTATCGTTCACAATTTTATTTTTTCATAATCAA 1620

1621 CTAAGGAAGAACGATCAATTGGATATAATCTTCTTACCAAAAATGATAGTTAAAATGTAT 1680

1681 ATATATCCTAGTCCCCTAACCaaATCCTGACCTATTGGGATACTTATAAAAATTTAAGTA 1740

1741 AGTGGGATACACAAAGAATAATAACTATTAACTTTTTCATTATTAGCcAAAAACCTAAGGG 1800

FIG.1B

1801 ATTTAAACTAATTGAAaCTGTATTTGATTGGACTTAATTTTTTATGTTTATTTAGAAGAT 1860
1861 AAAGATTTAAGAAGACCTTTACAATAAAGAGAAGAAATATCGAAGTCATTAATAAAGGA 1920
1921 GACTTACTTTTTATGACATTCTAATACTAAAAAATATAGAAATATTCCTTAATTCTAGAG 1980
1981 AAAGTAGTTTTACTAATTTTTTTACAACCTCAATAATACCATCACTGACACTTACCTTTAT 2040
2041 TAATTAGCTTCTAGAAAATAGCTGCTAATTAGGTTAATGAACATTTTACCTTAGTGAAAA 2100
2101 AAAaTTAATTAAATATGATTACAAAGTTGCACAGCATACTACTGAGAGGAAAGTGATTG 2160
2161 ATCTGTTTGTAATTACTTGTGTGATTGGTGTGTATAAAATACAAATTTACATTAAACTC 2220
2221 TAAAtcattaaaAAAAAAAAAAAAAAAAA 2247

FIG.1C

FIG. 2

1 GGCACGAGCCACCCTGCGTCGGGCCTCAGTCAGCCCCCGGGGAGGCCATGAACGCCAC 60
 1 M N A T 4
 61 GGGGACCCCGGTGGCCCCGAGTCCTGCCAACAGCTGGCGGCCGGCGGGCACAGCCGGCT 120
 5 G T P V A P E S C Q Q L A A G G H S R L 24
 121 CATTGTTCTGCACTACAACCACTCGGGCCGGCTGGCCGGGCGCGGGGGCCGGAGGATGG 180
 25 I V L H Y N H S G R L A G R G G P E D G 44
 181 CGGCCTGGGGGCCCTGCGGGGGCTGTCGGTGGCCGCCAGCTGCCTGGTGGTGCTGGAGAA 240
 45 G L G A L R G L S V A A S C L V V L E N 64
 241 CTTGCTGGTGCTGGCGGCCATCACCAGCCACATGCGGTGCAACGCTGGGTCTACTATTG 300
 65 L L V L A A I T S H M R S Q R W V Y Y C 84
 301 CCTGGTGAACATTACGATGAGTGACCTGCTCACGGGCGCGGCCTACCTGGCCAACGTGCT 360
 85 L V N I T M S D L L T G A A Y L A N V L 104
 361 GCTGTGCGGGGGCCCGCACCTTCCGTCTGGCGCCCGCCAGTGGTTCCTACGGAAGGGCCT 420
 105 L S G A R T F R L A P A Q W F L R K G L 124
 421 GCTCTTCACCGCCCTGGCCGCTCCACCTTCAGCCTGCTCTTCACTGCAGGGTTGCGCTT 480
 125 L F T A L A A S T F S L L F T A G L R F 144
 481 TGCCACCATGGTGC GGCCGGTGGCCGAGAGCGGGGCCACCAAGACCAGCCGCGTCTACGG 540
 145 A T M V R P V A E S G A T K T S R V Y G 164
 541 CTTTCATCGGCCTCTGCTGGCTGCTGGCCGCGCTGCTGGGGATGCTGCCTTTGCTGGGCTG 600
 165 F I G L C W L L A A L L G M L P L L G W 184
 601 GAACTGCCTGTGCGCCTTTGACCGCTGCTCCAGCCTTCTGCCCCTCTACTCCAAGCGCTA 660
 185 N C L C A F D R C S S L L P L Y S K R Y 204
 661 CATCCTCTTCTGCCTGGTGATCTTCGCCGGCGTCCTGGCCACCATCATGGGCCTCTATGG 720
 205 I L F C L V I F A G V L A T I M G L Y G 224
 721 GGCCATCTTCCGCCTGGTGCAGGCCAGCGGGCAGAAGGCCCCACGCCAGCGGGCCCGCCG 780
 225 A I F R L V Q A S G Q K A P R P A A R R 244

FIG.3A

781 CAAGGCCCGCCGCTGCTGAAGACGGTGCTGATGATCCTGCTGGCCTTCTTGGTGTGCTG 840
245 K A R R L L K T V L M I L L A F L V C W 264

841 GGGACCACTCTTCGGGCTGCTGCTGGCCGACGTCTTTGGCTCCAACCTCTGGGCCAGGA 900
265 G P L F G L L L A D V F G S N L W A Q E 284

901 GTACCTGCGGGGCATGGACTGGATCCTGGCCCTGGCCGTCCTCAACTCGGCGGTCAACCC 960
285 Y L R G M D W I L A L A V L N S A V N P 304

961 CATCATCTACTCCTTCCGCAGCAGGGAGGTGTGCAGAGCCGTGCTCAGCTTCCTCTGCTG 1020
305 I I Y S F R S R E V C R A V L S F L C C 324

1021 CGGGTGTCTCCGGCTGGGCATGCGAGGGCCCCGGGGACTGCCTGGCCCGGGCCGTGAGGC 1080
325 G C L R L G M R G P G D C L A R A V E A 344

1081 TCACTCCGGAGCTTCCACCACGACAGCTCTCTGAGGCCAAGGGACAGCTTTCGCGGCTC 1140
345 H S G A S T T D S S L R P R D S F R G S 364

1141 CCGCTCGCTCAGCTTTCGGATGCGGGAGCCCCTGTCCAGCATCTCCAGCGTGCGGAGCAT 1200
365 R S L S F R M R E P L S S I S S V R S I 384

1201 CTGAAGTTGCAGTCTTGCGTGTGGATGGTGAACCACCGGGTGCGTGCCAGGCAGGCCCT 1260
385 * 385

1261 CCTGGGGTACAGGAAGCTGTGTGCACGCAACCTCGCCCTGTATGGGGAGCAGGGAACGGG 1320

1321 ACAGGCCCCCATGGACTTGCCCGGTGGCCTCTCGGGGCTTCTGACGCCATATGGACTTGC 1380

1381 CCATTGCCTATGGCTCACCTGGACAAGGAGGCAACCACCCACCTCCCCGTAGGAGCAG 1440

1441 AGAGCACCTGGTGTGGGGGCGAGTGGGTTCCCCACAACCCGCTTCTGTGTGATTCTGG 1500

1501 GGAAGTCCCGGCCCTCTCTGGGCCTCAGTAGGGCTCCCAGGCTGCAAGGGGTGGACTGT 1560

1561 GGGATGCATGCCCTGGCAACATTGAAGTTCGATCATGGTAAAAAAAAAAAAAAAAAAAAA 1620

1621 AAAAAAAAAAAAAAAAAA 1637

FIG.3B

1 MNATGTPVAPESCQQLAAGGHSRLIVLHYNHSGRLAGRGGPEDGGLGALR 50
 |.:|.:|:.... :.. :. :|| |||..|:|.|: :. .
 1 MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNHTGKLNISADKEN.SIKLTS 49

51 GLSVAASCLVVLENLLVLAAITSHMRSQRWVYYCLVNITMSDLLTGAAYL 100
 .: : :|:|:|:|:|:|:| .| . :. :| :|| :. |:|:|:|:|:|:|.|.||
 50 VVFILICCFIILENIFVLLTIWTKKFHRPMYYFIGNLALSDDLAVAYT 99

101 ANVLLSGARTFRLAPAQWFLRKGLLFTALAASTFSLFTAGLRFATMVRP 150
 ||:||||| |:|:|:|:|:|:|. | :|.|.|.|.|.|.|. | |:|:|:|:|:
 100 ANLLLSGATTYKLTPAQWFLREGSMFVALSASFSLAIAIERYITMLKM 149

151 VAESGATKTSRVYGFILGCWLLAALLGMLPLLGNCLCAFDRCSSLLPLY 200
 ..|. .. |:|: |:|: ||:|. :|| ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 150 KLHNGS.NNFRLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLY 198

201 SKRYILFCLVIFAGVLATIMGLYGAI FRLVQASGQKAPRPAARRKARR.. 248
 |:|:|:|:|:|:|. |:|. :| .|:| ||. |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 199 HKHYILFCTTVFTLLLSIVILYCRIYSLVRTRSRLTFRKNISKASRSS 248

249LLKTVLMILLAFVLCWGPLFGLLLADVFGSNLWAQEYLRGMDWILA 294
 |||||:|:|:|. |:|. |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 249 ENVALLKTVIIVLSVFIACWAPLFILLLLDV.GCKVKTCDILFRAEYFLV 297

295 LAVLNSAVNPPIIYSFRSREVCRAVLSFLCCGCLRLGMRGPGDCLARAVEA 344
 |||||:|. |:|:|:|:|:|. :.:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 298 LAVLNSGTNPPIIYTLTNKEMRRAFIRIMSCCKCPSG..DSAGKFKRPIIA 345

345 ...HSGASTTDSSLRPRDSFRGSRSLSFMRREPLSSIS 379
 |:|:| :.:|. |... :.. :. :.:|:|
 346 GMEFSRSKSDNSSHPQKDE..GDNPETIMSSGNVNSSS 381

FIG.4